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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/943,002

DATE: 09/18/2001  
 TIME: 15:51:22

Input Set : A:\78973-1C seq 28-08-01 v1.txt  
 Output Set: N:\CRF3\09182001\I943002.raw

3 <110> APPLICANT: Duncan, Roy  
 5 <120> TITLE OF INVENTION: NOVEL REOVIRUS-DERIVED PROTEINS AND USES THEREFOR  
 7 <130> FILE REFERENCE: 78973-1C  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/943,002

C--> 10 <141> CURRENT FILING DATE: 2001-08-31

12 <160> NUMBER OF SEQ ID NOS: 15  
 14 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 1643

18 <212> TYPE: DNA

19 <213> ORGANISM: avian reovirus strain 176

21 <221> NAME/KEY: CDS

22 <222> LOCATION: (25)...(318)

23 <223> OTHER INFORMATION: nucleotide sequence encoding P11 protein (SEQ ID

26 <220> FEATURE:

27 <221> NAME/KEY: misc\_feature

28 <222> LOCATION: (293)...(730)

29 <223> OTHER INFORMATION: CDS encoding P16 protein (SEQ ID

30 NO:3)

32 <220> FEATURE:

33 <221> NAME/KEY: misc\_feature

34 <222> LOCATION: (630)...(1607)

35 <223> OTHER INFORMATION: CDS encoding sigma3 protein (SEQ

36 ID NO:4)

38 <400> SEQUENCE: 1

|    |   |     |
|----|---|-----|
| 39 | gctttttcaa tcccttggtc gtcg atg ctg cgt atg cct ccc ggt tcg tgt    | 51  |
| 40 | Met Leu Arg Met Pro Pro Gly Ser Cys                               |     |
| 41 | 1 5   |     |
| 43 | aac ggt gcg act gct gta ttt ggt aac gtt cat tgt cag gca gct caa   | 99  |
| 44 | Asn Gly Ala Thr Ala Val Phe Gly Asn Val His Cys Gln Ala Ala Gln   |     |
| 45 | 10 15 20 25   |     |
| 47 | aac acg gca ggt ggt gat ttg caa gct acg tca tcc ata att gca tat   | 147 |
| 48 | Asn Thr Ala Gly Gly Asp Leu Gln Ala Thr Ser Ser Ile Ile Ala Tyr   |     |
| 49 | 30 35 40  |     |
| 51 | tgg cct tat cta gcg gcg ggt ggt ggt ttc tta tta att gtt atc att   | 195 |
| 52 | Trp Pro Tyr Leu Ala Ala Gly Gly Gly Phe Leu Leu Ile Val Ile Ile   |     |
| 53 | 45 50 55  |     |
| 55 | ttc gct ctt cta tac tgt tgt aag gct aag gtc aag gcg gac gct gca   | 243 |
| 56 | Phe Ala Leu Leu Tyr Cys Cys Lys Ala Lys Val Lys Ala Asp Ala Ala   |     |
| 57 | 60 65 70  |     |
| 59 | cgt agt gtc ttc cat cgt gag ctg gta gcg ttg agt tct ggt aag cac   | 291 |
| 60 | Arg Ser Val Phe His Arg Glu Leu Val Ala Leu Ser Ser Gly Lys His   |     |
| 61 | 75 80 85  |     |
| 63 | aat gca atg gct ccg cca tac gac gtt tgaagtgcaa cgatttaatt         | 338 |
| 64 | Asn Ala Met Ala Pro Tyr Asp Val                                   |     |
| 65 | 90 95   |     |
| 67 | tctgtccgct atcacttcgc gaacttgcta tcccatcatt tactgctata actggggctg | 398 |

#2.  
 ENTERED

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68 acccatcaca gtattttaac attgagctcc cacacactca tcctctctat tccaaattgc 458
69 ctactctggt atctcaacct tgtagggtcc acgtgcggct gattcgccgg ttcgctctct 518
70 attcaacatt gtcaagtatt tgtgagtaag attgtgctct actattctcc ccacacgcta 578
71 tcgttccatt gcctgcatcc gatcgggcgg cttgtcttat agttcattgg gatggcgggt 638
72 ctcaatccat cgcagcgaag agagggtcgt agcttgatac tgtcattgac ttcgaacgtg 698
73 actataagtc atggcgattt gacgccgata tatgaacggc tgaccaatct agaagcgtct 758
74 acggagttat tacatcgctc catttccgat atatccacta ctgtctcaaa tatttctgca 818
75 aatttacaag acatgaccca taccttggat gatgtaactg ctaattttaga cggtttgagg 878
76 accactgtta ctgcaattca ggattccgtc tccattctgt ctacaaatgt gactgactta 938
77 acgaacacat cctctgcgca cgcggcgaca ctatcttcac ttcaaactac ggttgacgga 998
78 aactccactg ccatctccaa tttgaagagt gatgtatcgt cgaacgggtt agctattaca 1058
79 gatctgcagg atcgtgttaa atcattggag tctaccgcga gtcattggtc atctttttcg 1118
80 cctccgctta gtgtcgctga cggcgtgggt tcattagaca tggaccctca cttctgttct 1178
81 caacgagttt ctttaacatc ataactcgcg gaggtcaac taatgcaatt tcgggtggatg 1238
82 gcacggggta ctaacggatc atctgatacc attgacatga ccgttaacgc tcaactgtcat 1298
83 ggaagacgca ctgattatat gatgtcgtcc acgggaaatc tcacggtcac tagtaacgtc 1358
84 gtgttattaa ccttcgattt aagtgcata acgcataatc catcagacct agcacgtctt 1418
85 gttcccagtg cgggattcca agctgcgtcg ttccctgtgg acgtatcatt caccgcgat 1478
86 tctgcgactc atgcgtacca agcgtatggg gtgtactcga gctcacgtgt cttcacaatt 1538
87 actttcccaa ccggaggtga tggtaacagc aacattcgtt ccttgaccgt gcgtaccggc 1598
88 atcgacacct aagggtgtgg gccgtactgg gattggttat tcac 1643

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90 <210> SEQ ID NO: 2

91 <211> LENGTH: 98

92 <212> TYPE: PRT

93 <213> ORGANISM: avian reovirus strain 176

95 <400> SEQUENCE: 2

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96 Met Leu Arg Met Pro Gly Ser Cys Asn Gly Ala Thr Ala Val Phe
97 1 5 10 15
98 Gly Asn Val His Cys Gln Ala Ala Gln Asn Thr Ala Gly Gly Asp Leu
99 20 25 30
100 Gln Ala Thr Ser Ser Ile Ile Ala Tyr Trp Pro Tyr Leu Ala Ala Gly
101 35 40 45
102 Gly Gly Phe Leu Leu Ile Val Ile Ile Phe Ala Leu Leu Tyr Cys Cys
103 50 55 60
104 Lys Ala Lys Val Lys Ala Asp Ala Ala Arg Ser Val Phe His Arg Glu
105 65 70 75 80
106 Leu Val Ala Leu Ser Ser Gly Lys His Asn Ala Met Ala Pro Pro Tyr
107 85 90 95
108 Asp Val

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110 <210> SEQ ID NO: 3

111 <211> LENGTH: 146

112 <212> TYPE: PRT

113 <213> ORGANISM: avian reovirus strain 176

115 <400> SEQUENCE: 3

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116 Met Gln Trp Leu Arg His Thr Thr Phe Glu Val Gln Arg Phe Asn Phe
117 1 5 10 15
118 Cys Pro Leu Ser Leu Arg Glu Leu Ala Ile Pro Ser Phe Thr Ala Ile
119 20 25 30
120 Thr Gly Ala Asp Pro Ser Gln Tyr Phe Asn Ile Glu Leu Pro His Thr

```

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```

121          35          40          45
122 His Pro Leu Tyr Ser Lys Leu Pro Thr Leu Leu Ser Gln Pro Cys Arg
123          50          55          60
124 Val His Val Arg Leu Ile Arg Arg Phe Ala Leu Tyr Ser Thr Leu Ser
125 65          70          75          80
126 Ser Ile Cys Glu Tyr Asp Cys Ala Leu Leu Phe Ser Pro His Ala Ile
127          85          90          95
128 Val Pro Leu Pro Ala Ser Asp Arg Arg Ser Cys Leu Ile Val His Trp
129          100          105          110
130 Asp Gly Gly Ser Gln Ser Ile Ala Ala Lys Arg Gly Arg Gln Leu Asp
131          115          120          125
132 Thr Val Ile Asp Phe Glu Arg Asp Tyr Lys Ser Trp Arg Phe Asp Ala
133          130          135          140
134 Asp Leu
135 145
137 <210> SEQ ID NO: 4
138 <211> LENGTH: 326
139 <212> TYPE: PRT
140 <213> ORGANISM: avian reovirus strain 176
142 <400> SEQUENCE: 4
143 Met Ala Gly Leu Asn Pro Ser Gln Arg Arg Glu Val Val Ser Leu Ile
144 1          5          10          15
145 Leu Ser Leu Thr Ser Asn Val Thr Ile Ser His Gly Asp Leu Thr Pro
146          20          25          30
147 Ile Tyr Glu Arg Leu Thr Asn Leu Glu Ala Ser Thr Glu Leu Leu His
148          35          40          45
149 Arg Ser Ile Ser Asp Ile Ser Thr Thr Val Ser Asn Ile Ser Ala Asn
150          50          55          60
151 Leu Gln Asp Met Thr His Thr Leu Asp Asp Val Thr Ala Asn Leu Asp
152 65          70          75          80
153 Gly Leu Arg Thr Thr Val Thr Ala Leu Gln Asp Ser Val Ser Ile Leu
154          85          90          95
155 Ser Thr Asn Val Thr Asp Leu Thr Asn Thr Ser Ser Ala His Ala Ala
156          100          105          110
157 Thr Leu Ser Ser Leu Gln Thr Thr Val Asp Gly Asn Ser Thr Ala Ile
158          115          120          125
159 Ser Asn Leu Lys Ser Asp Val Ser Ser Asn Gly Leu Ala Ile Thr Asp
160          130          135          140
161 Leu Gln Asp Arg Val Lys Ser Leu Glu Ser Thr Ala Ser His Gly Leu
162 145          150          155          160
163 Ser Phe Ser Pro Pro Leu Ser Val Ala Asp Gly Val Val Ser Leu Asp
164          165          170          175
165 Met Asp Pro Tyr Phe Cys Ser Gln Arg Val Ser Leu Thr Ser Tyr Ser
166          180          185          190
167 Ala Glu Ala Gln Leu Met Gln Phe Arg Trp Met Ala Arg Gly Thr Asn
168          195          200          205
169 Gly Ser Ser Asp Thr Ile Asp Met Thr Val Asn Ala His Cys His Gly
170          210          215          220
171 Arg Arg Thr Asp Tyr Met Met Ser Ser Thr Gly Asn Leu Thr Val Thr

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```

172 225          230          235          240
173 Ser Asn Val Val Leu Leu Thr Phe Asp Leu Ser Asp Ile Thr His Ile
174          245          250          255
175 Pro Ser Asp Leu Ala Arg Leu Val Pro Ser Ala Gly Phe Gln Ala Ala
176          260          265          270
177 Ser Phe Pro Val Asp Val Ser Phe Thr Arg Asp Ser Ala Thr His Ala
178          275          280          285
179 Tyr Gln Ala Tyr Gly Val Tyr Ser Ser Ser Arg Val Phe Thr Ile Thr
180          290          295          300
181 Phe Pro Thr Gly Gly Asp Gly Thr Ala Asn Ile Arg Ser Leu Thr Val
182 305          310          315          320
183 Arg Thr Gly Ile Asp Thr
184          325
186 <210> SEQ ID NO: 5
187 <211> LENGTH: 1643
188 <212> TYPE: DNA
189 <213> ORGANISM: avian reovirus strain 138
191 <220> FEATURE:
192 <221> NAME/KEY: CDS
193 <222> LOCATION: (25)...(318)
194 <223> OTHER INFORMATION: nucleotide sequence encoding P11 protein (SEQ ID NO:6)
196 <220> FEATURE:
197 <221> NAME/KEY: misc_feature
198 <222> LOCATION: (293)...(730)
199 <223> OTHER INFORMATION: CDS encoding P16 protein (SEQ ID NO:7)
201 <220> FEATURE:
202 <221> NAME/KEY: misc_feature
203 <222> LOCATION: (630)...(1607)
204 <223> OTHER INFORMATION: CDS encoding sigma3 protein (SEQ ID NO:8)
206 <400> SEQUENCE: 5
207 gctttttcaa tcccttggtt gtcg atg ctg cgt atg cct ccc ggt tcg tgt      51
208          Met Leu Arg Met Pro Pro Gly Ser Cys
209          1          5
211 aac ggt gca aca gct atc ttt ggt aac gtc cat tgt cag gcg gct caa      99
212 Asn Gly Ala Thr Ala Ile Phe Gly Asn Val His Cys Gln Ala Ala Gln
213 10          15          20          25
215 aat act gcc ggc ggc gac ttg caa gct acc tca tcc ata att gcc tat      147
216 Asn Thr Ala Gly Gly Asp Leu Gln Ala Thr Ser Ser Ile Ile Ala Tyr
217          30          35          40
219 tgg cct tat cta gcg gcg ggt ggt ggt ttt ttg ttg att att att att      195
220 Trp Pro Tyr Leu Ala Ala Gly Gly Gly Phe Leu Leu Ile Ile Ile Ile
221          45          50          55
223 ttt gcc atc ttc tac tgt tgt aag gct aaa gtt aaa gcg gac gct gca      243
224 Phe Ala Ile Phe Tyr Cys Cys Lys Ala Lys Val Lys Ala Asp Ala Ala
225          60          65          70
227 cgg agt gtt ttc cac cgt gag ctt gta gca ctg agc tct ggt aag cac      291
228 Arg Ser Val Phe His Arg Glu Leu Val Ala Leu Ser Ser Gly Lys His
229          75          80          85
231 aat gca atg gct ccg cca tac gac gtt tgaagtgcaa cgctttgatt      338

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232 Asn Ala Met Ala Pro Pro Tyr Asp Val
233 90 95
235 tctgcccaat atcacttctgt gagcttgcca ccccatcggt tactgctata attgggattg 398
236 acccatcacg ttattttaat attgagcttt cgcacacgca tcctctctac tctaagttgc 458
237 cgactctggt atcgagcccc tgcgaggtcc acgtgctgtt gattcgtaga ttctctctct 518
238 gttcaacgct gtcgagtatc tgcgagtacg attgtgctgt actactttcc ccacacgcca 578
239 tcaactccact gtcctcatcc gatcagcgat cttatcttat agttcattgg gatggcggtg 638
240 ctcaatccat cacagcgaag agaggctgtc agcttgatac tgcattgac ttcgaacgcg 698
241 catataaatc atggcgattt gacgccaatc tatgaacggg tgaccagttt agaagcgtct 758
242 gcggaatcac tatatcgctc catttccagc atgtctacta ccgtttcaga catttcagca 818
243 gatttgcaga acgtgactcg cgccttggat gatgtgactg ctaattttaga tgggtatgaga 878
244 gtcaccatta ctacgcttca agattctgtg tccactctct caacgactgt aactgattta 938
245 aaaaacacct cttctgtgca ctcggaagca ctgtcttcac tccgaactat agttgatggg 998
246 aactccacta ccattgataa ttgaaaagt gatgtatcat caaacggctc tgctatcaca 1058
247 gacctgcaga gtcgtgttaa atccttggaa tctgtttcga gtcacgggct atctttttcg 1118
248 cctcctctta gtgtcgctga cgacgtagtg tcgttgagta tggaccctta cttttgctct 1178
249 cagcgagtca ccttgacatc atactcagca gaagctcaac tgatgcaatt ccaatggatg 1238
250 gcaagagggtg ctaacggatc atcagacact attgacatga ccgtcaatgc tcaactgtcat 1298
251 gggagacgca ctgattacat aatgtcgtcc acgggagggt ttacagttac tagtaatgcc 1358
252 gtgtctttta ctttcgactt gagttacatt acacgcctcc caccagacct ctgcgctctt 1418
253 gttcccagtg caggattcca agccgcgtcg ttccccgtgg atgtatcctt caccagagat 1478
254 tcgacaactc atacatatca agcttatgga gtgtattcta gttcgcgtgt atttaccatc 1538
255 actttcccga ctgggtgtga cgggtcccga aatatccgtt tctaaccgt gcgtaccggc 1598
256 atcgacacct aagggtgtggc gccgtacggg gattggttat tcatc 1643
258 <210> SEQ ID NO: 6
259 <211> LENGTH: 98
260 <212> TYPE: PRT
261 <213> ORGANISM: avian reovirus strain 138
263 <400> SEQUENCE: 6
264 Met Leu Arg Met Pro Pro Gly Ser Cys Asn Gly Ala Thr Ala Ile Phe
265 1 5 10 15
266 Gly Asn Val His Cys Gln Ala Ala Gln Asn Thr Ala Gly Gly Asp Leu
267 20 25 30
268 Gln Ala Thr Ser Ser Ile Ile Ala Tyr Trp Pro Tyr Leu Ala Ala Gly
269 35 40 45
270 Gly Gly Phe Leu Leu Ile Ile Ile Phe Ala Ile Phe Tyr Cys Cys
271 50 55 60
272 Lys Ala Lys Val Lys Ala Asp Ala Ala Arg Ser Val Phe His Arg Glu
273 65 70 75 80
274 Leu Val Ala Leu Ser Ser Gly Lys His Asn Ala Met Ala Pro Pro Tyr
275 85 90 95
276 Asp Val
278 <210> SEQ ID NO: 7
279 <211> LENGTH: 146
280 <212> TYPE: PRT
281 <213> ORGANISM: avian reovirus strain 138
283 <400> SEQUENCE: 7
284 Met Gln Trp Leu Arg His Thr Thr Phe Glu Val Gln Arg Phe Asp Phe
285 1 5 10 15

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VERIFICATION SUMMARY

DATE: 09/18/2001

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TIME: 15:51:23

Input Set : A:\78973-1C seq 28-08-01 v1.txt

Output Set: N:\CRF3\09182001\I943002.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date